

SEQUENCE LISTING

<110> Xu, Haiyan
Chen, Hong
Barnes, Glenn

<120> METHODS AND COMPOSITIONS FOR USE OF
INFLAMMATORY PROTEINS IN THE DIAGNOSIS AND TREATMENT OF
METABOLIC DISORDERS

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Thr Phe Leu Leu Gly Leu Pro Gly Asn	Gly Leu Val Leu Trp Val Ala	
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cac ttg gct ctc cag gga cag tgg ccc tac ggc agg ttc cta tgc aag 288
 His Leu Ala Leu Gln Gly Gln Trp Pro Tyr Gly Arg Phe Leu Cys Lys
 85 90 95

ctc atc ccc tcc atc att gtc ctc aac atg ttt gcc agt gtc ttc ctg 336
 Leu Ile Pro Ser Ile Ile Val Leu Asn Met Phe Ala Ser Val Phe Leu
 100 105 110

ctt act gcc att agc ctg gat cgc tgt ctt gtg gta ttc aag cca atc 384
 Leu Thr Ala Ile Ser Leu Asp Arg Cys Leu Val Val Phe Lys Pro Ile
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Trp Cys Gln Asn His Arg Asn Val Gly Met Ala Cys Ser Ile Cys Gly
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Cys Ile Trp Val Val Ala Phe Val Met Cys Ile Pro Val Phe Val Tyr
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Glu Asn Arg Ser Leu Glu Asn Ile Val Gln Pro Pro Gly Glu Met Asn			
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tca ctc cct agg ggt tct gct agg tta aca agt caa aat ctg tat tct		768	
Ser Leu Pro Arg Gly Ser Ala Arg Leu Thr Ser Gln Asn Leu Tyr Ser			
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Leu Leu Thr Asp Pro Glu Thr Pro Leu Gly Lys Thr Leu Met Ser Trp			
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tcc att cag gga att ctg gag gca gcc ttc agt gag gag ctc aca cgt		1392
Ser Ile Gln Gly Ile Leu Glu Ala Ala Phe Ser Glu Glu Leu Thr Arg		
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Thr Val *		

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Thr Phe Leu Leu Gly Leu Pro Gly Asn Gly Leu Val Leu Trp Val Ala			
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His Leu Ala Leu Gln Gly Gln Trp Pro Tyr Gly Arg Phe Leu Cys Lys			
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Arg Glu Ile Phe Thr Thr Asp Asn His Asn Arg Cys Gly Tyr Lys Phe			
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Gly Leu Ser Ser Leu Asp Tyr Pro Asp Phe Tyr Gly Asp Pro Leu			
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Glu Asn Arg Ser Leu Glu Asn Ile Val Gln Pro Pro Gly Glu Met Asn			
195	200	205	
Asp Arg Leu Asp Pro Ser Ser Phe Gln Thr Asn Asp His Pro Trp Thr			
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Val Pro Thr Val Phe Gln Pro Gln Thr Phe Gln Arg Pro Ser Ala Asp			
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Ser Leu Pro Arg Gly Ser Ala Arg Leu Thr Ser Gln Asn Leu Tyr Ser			
245	250	255	
Asn Val Phe Lys Pro Ala Asp Val Val Ser Pro Lys Ile Pro Ser Gly			
260	265	270	
Phe Pro Ile Glu Asp His Glu Thr Ser Pro Leu Asp Asn Ser Asp Ala			
275	280	285	
Phe Leu Ser Thr His Leu Lys Leu Phe Pro Ser Ala Ser Ser Asn Ser			
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Phe Tyr Glu Ser Glu Leu Pro Gln Gly Phe Gln Asp Tyr Tyr Asn Leu			
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Gly Gln Phe Thr Asp Asp Asp Gln Val Pro Thr Pro Leu Val Ala Ile			
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Thr Ile Thr Arg Leu Val Val Gly Phe Leu Leu Pro Ser Val Ile Met			
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																185
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Ser	His	Asp	Lys	Arg	Arg	Glu	Arg	Ala	Val	Ala	Ile	Val	Arg	Leu	Val	
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																200
																205
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Leu	Gly	Phe	Leu	Trp	Pro	Leu	Leu	Thr	Leu	Thr	Ile	Cys	Tyr	Thr	Phe	
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																220
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Ile	Leu	Leu	Arg	Thr	Trp	Ser	Arg	Arg	Ala	Thr	Arg	Ser	Thr	Lys	Thr	
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																230
																235
																240
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Leu	Lys	Val	Val	Val	Ala	Val	Val	Ala	Ser	Phe	Phe	Ile	Phe	Trp	Leu	
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																250
																255
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Pro	Tyr	Gln	Val	Thr	Gly	Ile	Met	Met	Ser	Phe	Leu	Glu	Pro	Ser	Ser	
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																265
																270
ccc	acc	ttc	ctg	ctg	aat	aag	ctg	gac	tcc	ctg	tgt	gtc	tcc	ttt		864
Pro	Thr	Phe	Leu	Leu	Leu	Asn	Lys	Leu	Asp	Ser	Leu	Cys	Val	Ser	Phe	
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																280
																285
gcc	tac	atc	aac	tgc	tgc	atc	aac	ccc	atc	atc	tac	gtg	gtg	gcc	ggc	912
Ala	Tyr	Ile	Asn	Cys	Cys	Ile	Asn	Pro	Ile	Ile	Tyr	Val	Val	Ala	Gly	
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																295
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Gln	Gly	Phe	Gln	Gly	Arg	Leu	Arg	Lys	Ser	Leu	Pro	Ser	Leu	Leu	Arg	
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																310
																315
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																105
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Ser	His	Asp	Lys	Arg	Arg	Glu	Arg	Ala	Val	Ala	Ile	Val	Arg	Leu	Val
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Leu	Gly	Phe	Leu	Trp	Pro	Leu	Leu	Thr	Ile	Cys	Tyr	Thr	Phe		
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Pro	Tyr	Gln	Val	Thr	Gly	Ile	Met	Met	Ser	Phe	Leu	Glu	Pro	Ser	Ser
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Pro	Thr	Phe	Leu	Leu	Leu	Asn	Lys	Leu	Asp	Ser	Leu	Cys	Val	Ser	Phe
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Thr	Asp	Ile	Ala	Asp	Asp	Gly	Cys	Pro	Lys	Pro	Pro	Glu	Ile	Ala	His
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Gly	Tyr	Val	Glu	His	Ser	Val	Arg	Tyr	Gln	Cys	Lys	Asn	Tyr	Tyr	Lys
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Ser Ile Gln Asp Trp Val Gln Lys Thr Ile Ala Glu Asn *	
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Asp Lys Leu Pro Glu Cys Glu Ala Asp Asp Gly Cys Pro Lys Pro Pro	
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Ala Lys Met Val Ser His His Asn Leu Thr Thr Gly Ala Thr Leu Ile	
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Ser Glu Asn Ala Thr Ala Lys Asp Ile Ala Pro Thr Leu Thr Leu Tyr	
210 215 220	
Val Gly Lys Lys Gln Leu Val Glu Ile Glu Lys Val Val Leu His Pro	
225 230 235 240	
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325 330 335	
His Thr Phe Cys Ala Gly Met Ser Lys Tyr Gln Glu Asp Thr Cys Tyr	
340 345 350	
Gly Asp Ala Gly Ser Ala Phe Ala Val His Asp Leu Glu Glu Asp Thr	
355 360 365	
Trp Tyr Ala Thr Gly Ile Leu Ser Phe Asp Lys Ser Cys Ala Val Ala	
370 375 380	
Glu Tyr Gly Val Tyr Val Lys Val Thr Ser Ile Gln Asp Trp Val Gln	
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Lys Thr Ile Ala Glu Asn	

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 aacggcacc aaggaaaact cactacc atg aga att gca gtg att tgc ttt tgc 114
 Met Arg Ile Ala Val Ile Cys Phe Cys
 1 5

ctc cta ggc atc acc tgt gcc ata cca gtt aaa cag gct gat tct gga	162
Leu Leu Gly Ile Thr Cys Ala Ile Pro Val Lys Gln Ala Asp Ser Gly	
10 15 20 25	
agt tct gag gaa aag cag ctt tac aac aaa tac cca gat gct gtg gcc	210
Ser Ser Glu Glu Lys Gln Leu Tyr Asn Lys Tyr Pro Asp Ala Val Ala	
30 35 40	
aca tgg cta aac cct gac cca tct cag aag cag aat ctc cta gcc cca	258
Thr Trp Leu Asn Pro Asp Pro Ser Gln Lys Gln Asn Leu Leu Ala Pro	
45 50 55	
cag acc ctt cca agt aag tcc aac gaa agc cat gac cac atg gat gat	306
Gln Thr Leu Pro Ser Lys Ser Asn Glu Ser His Asp His Met Asp Asp	
60 65 70	
atg gat gat gaa gat gat gat gac cat gtg gac agc cag gac tcc att	354
Met Asp Asp Glu Asp Asp Asp His Val Asp Ser Gln Asp Ser Ile	
75 80 85	
gac tcg aac gac tct gat gat gta gat gac act gat gat tct cac cag	402
Asp Ser Asn Asp Ser Asp Asp Val Asp Asp Thr Asp Asp Ser His Gln	
90 95 100 105	
tct gat gag tct cac cat tct gat gaa tct gat gaa ctg gtc act gat	450
Ser Asp Glu Ser His His Ser Asp Glu Ser Asp Glu Leu Val Thr Asp	
110 115 120	
ttt ccc acg gac ctg cca gca acc gaa gtt ttc act cca gtt gtc ccc	498
Phe Pro Thr Asp Leu Pro Ala Thr Glu Val Phe Thr Pro Val Val Pro	
125 130 135	
aca gta gac aca tat gat ggc cga ggt gat agt gtg gtt tat gga ctg	546
Thr Val Asp Thr Tyr Asp Gly Arg Gly Asp Ser Val Val Tyr Gly Leu	
140 145 150	
agg tca aaa tct aag aag ttt cgc aga cct gac atc cag tac cct gat	594
Arg Ser Lys Ser Lys Lys Phe Arg Arg Pro Asp Ile Gln Tyr Pro Asp	
155 160 165	
gct aca gac gag gac atc acc tca cac atg gaa agc gag gag ttg aat	642
Ala Thr Asp Glu Asp Ile Thr Ser His Met Glu Ser Glu Glu Leu Asn	
170 175 180 185	
ggt gca tac aag gcc atc ccc gtt gcc cag gac ctg aac gcg cct tct	690
Gly Ala Tyr Lys Ala Ile Pro Val Ala Gln Asp Leu Asn Ala Pro Ser	
190 195 200	
gat tgg gac agc cgt ggg aag gac agt tat gaa acg agt cag ctg gat	738
Asp Trp Asp Ser Arg Gly Lys Asp Ser Tyr Glu Thr Ser Gln Leu Asp	
205 210 215	

gac cag agt gct gaa acc cac agc cac aag cag tcc aga tta tat aag	786
Asp Gln Ser Ala Glu Thr His Ser His Lys Gln Ser Arg Leu Tyr Lys	
220 225 230	
cgg aaa gcc aat gat gag agc aat gag cat tcc gat gtg att gat agt	834
Arg Lys Ala Asn Asp Glu Ser Asn Glu His Ser Asp Val Ile Asp Ser	
235 240 245	
cag gaa ctt tcc aaa gtc agc cgt gaa ttc cac agc cat gaa ttt cac	882
Gln Glu Leu Ser Lys Val Ser Arg Glu Phe His Ser His Glu Phe His	
250 255 260 265	
agc cat gaa gat atg ctg gtt gta gac ccc aaa agt aag gaa gaa gat	930
Ser His Glu Asp Met Leu Val Val Asp Pro Lys Ser Lys Glu Glu Asp	
270 275 280	
aaa cac ctg aaa ttt cgt att tct cat gaa tta gat agt gca tct tct	978
Lys His Leu Lys Phe Arg Ile Ser His Glu Leu Asp Ser Ala Ser Ser	
285 290 295	
gag gtc aat taa aaggagaaaa aataacaattt ctcactttgc attttagtcaa	1030
Glu Val Asn *	
300	
aagaaaaaat gccttatagc aaaatgaaag agaacatgaa atgcttcttt ctcagtttat	1090
tggttgaatg tgatctatt tgagtctgga aataactaat gtgtttgata attagtttag	1150
tttgggctt catggaaact ccctgtaaac taaaagcttc agggttatgt ctatgttcat	1210
tctatagaag aaatgcacaaac tatcactgtt tttaatatt tggatttctc tcattgtatag	1270
aaatttatgt agaagcaacaaaactt taccctactt aaaagagaat ataacatttt	1330
atgtcactt aatcttttggtt ttttaagtt agtgtatatt ttgtgtgtat tatcttttg	1390
tgggtgtat aatatcttttta tcttgaatgt aataagaatt tgggtgtgtc aattgcttat	1450
ttgtttcccc acgggttgtcc agcaattaat aaaacataac ctttttact gcctaaaaaa	1510
aaaaaaaaaaaa aaaa	1524
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Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu	
20 25 30	
Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro	
35 40 45	
Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser	
50 55 60	
Asn Glu Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp	
65 70 75 80	
Asp His Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp	
85 90 95	
Val Asp Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser	
100 105 110	
Asp Glu Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala	
115 120 125	
Thr Glu Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly	
130 135 140	
Arg Gly Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe	
145 150 155 160	
Arg Arg Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr	
165 170 175	
Ser His Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro	
180 185 190	
Val Ala Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys	
195 200 205	
Asp Ser Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His	
210 215 220	

Ser His Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser
 225 230 235 240
 Asn Glu His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser
 245 250 255
 Arg Glu Phe His Ser His Glu Phe His Ser His Glu Asp Met Leu Val
 260 265 270
 Val Asp Pro Lys Ser Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile
 275 280 285
 Ser His Glu Leu Asp Ser Ala Ser Ser Glu Val Asn
 290 295 300

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 <211> 2657
 <212> DNA
 <213> mouse

<220>
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 <222> (589)...(2022)

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 gcactcagaa gacggaggca ggagaatcat agcttcaggc cagcctcttca tacaatata 180
 tcagttggaa gtcagccagc ttagacaaca tggagagcct gtggcggaaag ccactggta 240
 agccccaaatc tcagtagcag agagctgccc agggtgcgta ctgcaaaaaaaaaaa 300
 acaacagaag tagggaggtg taaaataaag ttttaggggggg tggaaatttaa gctgatgtgg 360
 acttccaaat aaagttaacc ttttagatacc tatttaaatc aatagcatag acctgaaact 420
 gtctatcaga aaatgtgtct attctgagga aggagtgcata acgagggtct gtgagggggg 480
 cctctggctt ttaggggttg taccatcaca taagactcct aaaagcacat acttttataa 540
 attcaccatg agcttaaca tcttctttgt catttcgcag actgagcc atg gag tct 597
 Met Glu Ser
 1

ttc gat gct gac acc aat tca act gac cta cac tca cgg cct ctg ttt 645
 Phe Asp Ala Asp Thr Asn Ser Thr Asp Leu His Ser Arg Pro Leu Phe
 5 10 15

caa ccc caa gac att gcc tcc atg gtc att ctt ggt ctc act tgt cta 693
 Gln Pro Gln Asp Ile Ala Ser Met Val Ile Leu Gly Leu Thr Cys Leu
 20 25 30 35

ttg gga ctg cta ggc aat ggg ctg gtg ctg tgg gta gct ggc gta aag 741
 Leu Gly Leu Leu Gly Asn Gly Leu Val Leu Trp Val Ala Gly Val Lys
 40 45 50

atg aag acg acc gtg aac aca gtc tgg ttc ctc cat ctc acc ctg gcc 789
 Met Lys Thr Thr Val Asn Thr Val Trp Phe Leu His Leu Thr Leu Ala
 55 60 65

gat ttc ctc tgc tgc ctc tcc ttg ccc ttc tcc ttg gct cac ctg att 837
 Asp Phe Leu Cys Cys Leu Ser Leu Pro Phe Ser Leu Ala His Leu Ile
 70 75 80

ctc caa gga cac tgg ccc tat ggc ttg ttc ctg tgc aaa ctt atc cca 885
 Leu Gln Gly His Trp Pro Tyr Gly Leu Phe Leu Cys Lys Leu Ile Pro
 85 90 95

tcc atc att att ctc aac atg ttt gcc agt gtc ttc ctg ctt act gcc 933
 Ser Ile Ile Ile Leu Asn Met Phe Ala Ser Val Phe Leu Leu Thr Ala
 100 105 110 115

att agc ctg gac cga tgt ctg ata gta cat aag cca atc tgg tgc cag 981
 Ile Ser Leu Asp Arg Cys Leu Ile Val His Lys Pro Ile Trp Cys Gln
 120 125 130

aat cat cga aac gtg aga acc gcc ttc gcc atc tgt gga tgt gtc tgg 1029
 Asn His Arg Asn Val Arg Thr Ala Phe Ala Ile Cys Gly Cys Val Trp

135	140	145	
gtg gta gcc ttt gtg atg tgt gtg ccc gta ttt gta tac cgt gat ctg Val Val Ala Phe Val Met Cys Val Pro Val Phe Val Tyr Arg Asp Leu 150 155 160			1077
ttc att atg gac aat cgc agt ata tgt aga tat aat ttt gat tcc tcc Phe Ile Met Asp Asn Arg Ser Ile Cys Arg Tyr Asn Phe Asp Ser Ser 165 170 175			1125
agg tca tat gat tat tgg gac tac gtg tac aaa cta agt cta cca gaa Arg Ser Tyr Asp Tyr Trp Asp Tyr Val Tyr Lys Leu Ser Leu Pro Glu 180 185 190 195			1173
agc aat tct act gat aac tcc act gct cag cta act gga cat atg aat Ser Asn Ser Thr Asp Asn Ser Thr Ala Gln Leu Thr Gly His Met Asn 200 205 210			1221
gac agg tca gct cct tcc tct gta cag gca agg gat tac ttt tgg aca Asp Arg Ser Ala Pro Ser Ser Val Gln Ala Arg Asp Tyr Phe Trp Thr 215 220 225			1269
gtt acc act gcc ctc cag tca cag cca ttc cta aca tct cct gaa gac Val Thr Ala Leu Gln Ser Gln Pro Phe Leu Thr Ser Pro Glu Asp 230 235 240			1317
tca ttc tct cta gat tca gca aac caa caa ccc cat tat ggt gga aag Ser Phe Ser Leu Asp Ser Ala Asn Gln Gln Pro His Tyr Gly Gly Lys 245 250 255			1365
cct cct aat gtc ctc aca gcc gcc gta ccc agc ggg ttt cct gtt gaa Pro Pro Asn Val Leu Thr Ala Ala Val Pro Ser Gly Phe Pro Val Glu 260 265 270 275			1413
gat cgt aaa tcc aat aca ctg aac gct gac gct ttt ctc tct gct cac Asp Arg Lys Ser Asn Thr Leu Asn Ala Asp Ala Phe Leu Ser Ala His 280 285 290			1461
aca gaa ctt ttc cct act gct tct agt ggt cat tta tac ccc tat gat Thr Glu Leu Phe Pro Thr Ala Ser Ser Gly His Leu Tyr Pro Tyr Asp 295 300 305			1509
ttc cag ggg gat tat gtt gac caa ttc acg tat gac aat cat gtg ccg Phe Gln Gly Asp Tyr Val Asp Gln Phe Thr Tyr Asp Asn His Val Pro 310 315 320			1557
aca ccg ctg atg gca ata acc atc aca agg ctg gtg gtg ggc ttc ctg Thr Pro Leu Met Ala Ile Thr Ile Thr Arg Leu Val Val Gly Phe Leu 325 330 335			1605
gtg ccg ttt ttc atc atg gta att tgt tac agc ctc atc gtc ttc aga Val Pro Phe Phe Ile Met Val Ile Cys Tyr Ser Leu Ile Val Phe Arg 340 345 350 355			1653
atg cga aaa acc aac ttc acc aag tct cggt aac aaa acc ttt cggt gtg Met Arg Lys Thr Asn Phe Thr Lys Ser Arg Asn Lys Thr Phe Arg Val 360 365 370			1701
gct gtg gct gtg gtc act gtc ttt ttc atc tgc tgg act cca tac cat Ala Val Ala Val Val Thr Val Phe Phe Ile Cys Trp Thr Pro Tyr His 375 380 385			1749
ctt gtc gga gtc ctg cta ttg att act gat cca gaa agt tcc ttg ggg Leu Val Gly Val Leu Leu Ile Thr Asp Pro Glu Ser Ser Leu Gly 390 395 400			1797
gaa gct gtg atg tcc tgg gac cac atg tcc att gct tta gca tct gcc Glu Ala Val Met Ser Trp Asp His Met Ser Ile Ala Leu Ala Ser Ala 405 410 415			1845

aat agt tgc ttc aac cct ttc ctg tat gcc ctc ttg ggg aaa gac ttt 1893
 Asn Ser Cys Phe Asn Pro Phe Leu Tyr Ala Leu Leu Gly Lys Asp Phe
 420 425 430 435
 agg aag aaa gca aga cag tct ata aag ggc att ctg gaa gca gcc ttc 1941
 Arg Lys Lys Ala Arg Gln Ser Ile Lys Gly Ile Leu Glu Ala Ala Phe
 440 445 450
 agc gaa gag ctc acg cac tct acc aac tgt acc caa gac aaa gcc tct 1989
 Ser Glu Glu Leu Thr His Ser Thr Asn Cys Thr Gln Asp Lys Ala Ser
 455 460 465
 tca aaa aga aac aat atg agt aca gat gtg tga agatgtggcc ctggAACCT 2042
 Ser Lys Arg Asn Asn Met Ser Thr Asp Val *
 470 475
 aagcagagtt ctcaggtaaa cagtgtgaa tgacatgtga gcaggacact ttagacaatt 2102
 tggcgactct cagagaaaagg tctcttattt acatcagcat cattgaaaaa cattaaagat 2162
 gcaaaaatttcc aagccccatcc ccagatgtgt tgactcagaa tctctggccc atgggaccag 2222
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 <212> PRT
 <213> mouse

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 Pro Leu Phe Gln Pro Gln Asp Ile Ala Ser Met Val Ile Leu Gly Leu
 20 25 30
 Thr Cys Leu Leu Gly Leu Leu Gly Asn Gly Leu Val Leu Trp Val Ala
 35 40 45
 Gly Val Lys Met Lys Thr Thr Val Asn Thr Val Trp Phe Leu His Leu
 50 55 60
 Thr Leu Ala Asp Phe Leu Cys Cys Leu Ser Leu Pro Phe Ser Leu Ala
 65 70 75 80
 His Leu Ile Leu Gln Gly His Trp Pro Tyr Gly Leu Phe Leu Cys Lys
 85 90 95
 Leu Ile Pro Ser Ile Ile Ile Leu Asn Met Phe Ala Ser Val Phe Leu
 100 105 110
 Leu Thr Ala Ile Ser Leu Asp Arg Cys Leu Ile Val His Lys Pro Ile
 115 120 125
 Trp Cys Gln Asn His Arg Asn Val Arg Thr Ala Phe Ala Ile Cys Gly
 130 135 140
 Cys Val Trp Val Val Ala Phe Val Met Cys Val Pro Val Phe Val Tyr
 145 150 155 160
 Arg Asp Leu Phe Ile Met Asp Asn Arg Ser Ile Cys Arg Tyr Asn Phe
 165 170 175
 Asp Ser Ser Arg Ser Tyr Asp Tyr Trp Asp Tyr Val Tyr Lys Leu Ser
 180 185 190
 Leu Pro Glu Ser Asn Ser Thr Asp Asn Ser Thr Ala Gln Leu Thr Gly
 195 200 205
 His Met Asn Asp Arg Ser Ala Pro Ser Ser Val Gln Ala Arg Asp Tyr
 210 215 220
 Phe Trp Thr Val Thr Thr Ala Leu Gln Ser Gln Pro Phe Leu Thr Ser
 225 230 235 240
 Pro Glu Asp Ser Phe Ser Leu Asp Ser Ala Asn Gln Gln Pro His Tyr
 245 250 255
 Gly Gly Lys Pro Pro Asn Val Leu Thr Ala Ala Val Pro Ser Gly Phe
 260 265 270

Pro Val Glu Asp Arg Lys Ser Asn Thr Leu Asn Ala Asp Ala Phe Leu
 275 280 285
 Ser Ala His Thr Glu Leu Phe Pro Thr Ala Ser Ser Gly His Leu Tyr
 290 295 300
 Pro Tyr Asp Phe Gln Gly Asp Tyr Val Asp Gln Phe Thr Tyr Asp Asn
 305 310 315 320
 His Val Pro Thr Pro Leu Met Ala Ile Thr Ile Thr Arg Leu Val Val
 325 330 335
 Gly Phe Leu Val Pro Phe Phe Ile Met Val Ile Cys Tyr Ser Leu Ile
 340 345 350
 Val Phe Arg Met Arg Lys Thr Asn Phe Thr Lys Ser Arg Asn Lys Thr
 355 360 365
 Phe Arg Val Ala Val Ala Val Thr Val Phe Phe Ile Cys Trp Thr
 370 375 380
 Pro Tyr His Leu Val Gly Val Leu Leu Ile Thr Asp Pro Glu Ser
 385 390 395 400
 Ser Leu Gly Glu Ala Val Met Ser Trp Asp His Met Ser Ile Ala Leu
 405 410 415
 Ala Ser Ala Asn Ser Cys Phe Asn Pro Phe Leu Tyr Ala Leu Leu Gly
 420 425 430
 Lys Asp Phe Arg Lys Lys Ala Arg Gln Ser Ile Lys Gly Ile Leu Glu
 435 440 445
 Ala Ala Phe Ser Glu Glu Leu Thr His Ser Thr Asn Cys Thr Gln Asp
 450 455 460
 Lys Ala Ser Ser Lys Arg Asn Asn Met Ser Thr Asp Val
 465 470 475

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 <211> 1109
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (84)...(1085)

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 tcaactatga tcactatgga acc atg gat cct aac ata cct gcg gat ggc att 113
 Met Asp Pro Asn Ile Pro Ala Asp Gly Ile
 1 5 10

cac ctc ccg aag cgg caa cct ggg gat gtt gca gcc ctt atc atc tac	161
His Leu Pro Lys Arg Gln Pro Gly Asp Val Ala Ala Leu Ile Ile Tyr	
15 20 25	

tcg gtg gtg ttc ctg gtg gga gta ccc ggg aat gcc ctg gtg gtg tgg 209
 Ser Val Val Phe Leu Val Gly Val Pro Gly Asn Ala Leu Val Val Trp
 30 35 40

gtg aca gcc ttc gag cca gac ggg ccc tca aac gcc atc tgg ttt ctg	257
Val Thr Ala Phe Glu Pro Asp Gly Pro Ser Asn Ala Ile Trp Phe Leu	
45 50 55	

aat ctg gcg gtg gcc gac ctc ctc tgc ttg gcc atg cct gtc ctg 305
 Asn Leu Ala Val Ala Asp Leu Leu Ser Cys Leu Ala Met Pro Val Leu
 60 65 70

ttc acg acc gtt tta aat cat aac tac tgg tac ttt gat gcc acc gcc	353
Phe Thr Thr Val Leu Asn His Asn Tyr Trp Tyr Phe Asp Ala Thr Ala	
75 80 85 90	

tgt ata gtc ctg ccc tcg ctc atc ctg ctc aac atg tac gcc agt atc 401
 Cys Ile Val Leu Pro Ser Leu Ile Leu Leu Asn Met Tyr Ala Ser Ile
 95 100 105

ctg ctg ctg gct acc att agt gcc gac cgt ttc ctg ctg gtg ttc aag	449
Leu Leu Leu Ala Thr Ile Ser Ala Asp Arg Phe Leu Val Phe Lys	

110	115	120	
ccc atc tgg tgt cag aag gtc cgc ggg act ggc ctg gca tgg atg gcc Pro Ile Trp Cys Gln Lys Val Arg Gly Thr Gly Leu Ala Trp Met Ala 125	130	135	497
tgt gga gtg gcc tgg gtc tta gca ttg ctc acc att cca tcc ttc Cys Gly Val Ala Trp Val Leu Ala Leu Leu Thr Ile Pro Ser Phe 140	145	150	545
gtg tac cgg gag gca tat aag gac ttc tac tca gag cac act gta tgt Val Tyr Arg Glu Ala Tyr Lys Asp Phe Tyr Ser Glu His Thr Val Cys 155	160	165	593
ggt att aac tat ggt ggg ggt agc ttc ccc aaa gag aag gct gtg gcc Gly Ile Asn Tyr Gly Gly Ser Phe Pro Lys Glu Lys Ala Val Ala 175	180	185	641
atc ctg cgg ctg atg gtg ggt ttt gtg ttg cct ctg ctc act cta aac Ile Leu Arg Leu Met Val Gly Phe Val Leu Pro Leu Leu Thr Leu Asn 190	195	200	689
atc tgc tac acc ttc ctc ctg ctc cgg acc tgg agt cgc aag gcc acg Ile Cys Tyr Thr Phe Leu Leu Leu Arg Thr Trp Ser Arg Lys Ala Thr 205	210	215	737
cgc tcc acc aag acg ctc aaa gtg gtg atg gct gtg gtc atc tgt ttc Arg Ser Thr Lys Thr Leu Lys Val Val Met Ala Val Val Ile Cys Phe 220	225	230	785
ttt atc ttc tgg ctg ccc tat cag gtg acc ggg gtg atg ata gcg tgg Phe Ile Phe Trp Leu Pro Tyr Gln Val Thr Gly Val Met Ile Ala Trp 235	240	245	833
ctg ccc ccg tcc tcg ccc acc ttg aag agg gtg gag aag ctg aac tcc Leu Pro Pro Ser Ser Pro Thr Leu Lys Arg Val Glu Lys Leu Asn Ser 255	260	265	881
ctg tgc gtg tcc ctg gcc tac atc aac tgc tgt gtt aac cct atc atc Leu Cys Val Ser Leu Ala Tyr Ile Asn Cys Cys Val Asn Pro Ile Ile 270	275	280	929
tac gtc atg gct ggc cag ggt ttc cat gga cga ctc cta agg tct ctc Tyr Val Met Ala Gly Gln Gly Phe His Gly Arg Leu Leu Arg Ser Leu 285	290	295	977
ccc agc atc ata cga aac gct ctc tct gag gat tca gtg ggc agg gat Pro Ser Ile Ile Arg Asn Ala Leu Ser Glu Asp Ser Val Gly Arg Asp 300	305	310	1025
agc aag act ttc act ccg tcc aca gac gac acc tca acc cgg aag agt Ser Lys Thr Phe Thr Pro Ser Thr Asp Asp Thr Ser Thr Arg Lys Ser 315	320	325	1073
cag gcg gtg tag aggagaagcc acaactggcc tagc Gln Ala Val *			1109

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<211> 333
<212> PRT
<213> mouse

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Met Asp Pro Asn Ile Pro Ala Asp Gly Ile His Leu Pro Lys Arg Gln
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Pro Gly Asp Val Ala Ala Leu Ile Ile Tyr Ser Val Val Phe Leu Val
20 25 30

Gly	Val	Pro	Gly	Asn	Ala	Leu	Val	Val	Trp	Val	Thr	Ala	Phe	Glu	Pro
35						40					45				
Asp	Gly	Pro	Ser	Asn	Ala	Ile	Trp	Phe	Leu	Asn	Leu	Ala	Val	Ala	Asp
50						55					60				
Leu	Leu	Ser	Cys	Leu	Ala	Met	Pro	Val	Leu	Phe	Thr	Thr	Val	Leu	Asn
65						70				75					80
His	Asn	Tyr	Trp	Tyr	Phe	Asp	Ala	Thr	Ala	Cys	Ile	Val	Leu	Pro	Ser
						85				90					95
Leu	Ile	Leu	Leu	Asn	Met	Tyr	Ala	Ser	Ile	Leu	Leu	Leu	Ala	Thr	Ile
						100			105						110
Ser	Ala	Asp	Arg	Phe	Leu	Leu	Val	Phe	Lys	Pro	Ile	Trp	Cys	Gln	Lys
						115			120			125			
Val	Arg	Gly	Thr	Gly	Leu	Ala	Trp	Met	Ala	Cys	Gly	Val	Ala	Trp	Val
						130			135			140			
Leu	Ala	Leu	Leu	Leu	Thr	Ile	Pro	Ser	Phe	Val	Tyr	Arg	Glu	Ala	Tyr
145						150				155					160
Lys	Asp	Phe	Tyr	Ser	Glu	His	Thr	Val	Cys	Gly	Ile	Asn	Tyr	Gly	Gly
						165			170						175
Gly	Ser	Phe	Pro	Lys	Glu	Lys	Ala	Val	Ala	Ile	Leu	Arg	Leu	Met	Val
						180			185			190			
Gly	Phe	Val	Leu	Pro	Leu	Leu	Thr	Leu	Asn	Ile	Cys	Tyr	Thr	Phe	Leu
						195			200			205			
Leu	Leu	Arg	Thr	Trp	Ser	Arg	Lys	Ala	Thr	Arg	Ser	Thr	Lys	Thr	Leu
						210			215			220			
Lys	Val	Val	Met	Ala	Val	Val	Ile	Cys	Phe	Phe	Ile	Phe	Trp	Leu	Pro
225						230				235					240
Tyr	Gln	Val	Thr	Gly	Val	Met	Ile	Ala	Trp	Leu	Pro	Pro	Ser	Ser	Pro
						245			250						255
Thr	Leu	Lys	Arg	Val	Glu	Lys	Leu	Asn	Ser	Leu	Cys	Val	Ser	Leu	Ala
						260			265			270			
Tyr	Ile	Asn	Cys	Cys	Val	Asn	Pro	Ile	Ile	Tyr	Val	Met	Ala	Gly	Gln
						275			280			285			
Gly	Phe	His	Gly	Arg	Leu	Leu	Arg	Ser	Leu	Pro	Ser	Ile	Ile	Arg	Asn
						290			295			300			
Ala	Leu	Ser	Glu	Asp	Ser	Val	Gly	Arg	Asp	Ser	Lys	Thr	Phe	Thr	Pro
305						310				315					320
Ser	Thr	Asp	Asp	Thr	Ser	Thr	Arg	Lys	Ser	Gln	Ala	Val			
						325			330						

<210> 13
<211> 1267
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (49) . . . (1092)

<400> 13

gaattcggca cgagcagccc ttccagagag aggcaagaga ggtccacg atg aga gcc
Met Arg Ala
1

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ctg gga gct gtt gtc act ctc ctg ctc tgg ggt cag ctt ttt gct gtg 105
Leu Gly Ala Val Val Thr Leu Leu Leu Trp Gly Gln Leu Phe Ala Val
      5           10          15

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gag ttg ggc aat gat gcc atg gac ttt gaa gat gac agc tgc cca aag 153
 Glu Leu Gly Asn Asp Ala Met Asp Phe Glu Asp Asp Ser Cys Pro Lys
 20 25 30 35

ccc cca gag att gca aac ggc tat gtg gag cac ttg gtt cgc tat cgc 201
 Pro Pro Glu Ile Ala Asn Gly Tyr Val Glu His Leu Val Arg Tyr Arg
 40 45 50

tgc cga cag ttc tac aga cta cg^g gcc gaa g^ga gat g^gg gt^g tac acc 249
 Cys Arg Gln Phe Tyr Arg Leu Arg Ala Glu Gly Asp Gly Val Tyr Thr
 55 60 65

tta aac gac gag aag caa tgg gtg aac aca gtc gct gga gag aaa ctc Leu Asn Asp Glu Lys Gln Trp Val Asn Thr Val Ala Gly Glu Lys Leu	297
70 75 80	
ccc gaa tgt gag gca gtg tgt ggg aag ccc aag cac cct gtg gac cag Pro Glu Cys Glu Ala Val Cys Gly Lys Pro Lys His Pro Val Asp Gln	345
85 90 95	
gtg cag cgc atc atc ggt ggc tct atg gat gcc aaa ggc agc ttt cct Val Gln Arg Ile Ile Gly Gly Ser Met Asp Ala Lys Gly Ser Phe Pro	393
100 105 110 115	
tgg cag gcc aag atg atc tcc cgc cac gga ctc acc acc ggg gcc acg Trp Gln Ala Lys Met Ile Ser Arg His Gly Leu Thr Thr Gly Ala Thr	441
120 125 130	
ttg atc agt gac cag tgg ctg ctg acc acg gcc aaa aac ctc ttc ctg Leu Ile Ser Asp Gln Trp Leu Leu Thr Thr Ala Lys Asn Leu Phe Leu	489
135 140 145	
aac cac agc gag acg gcg tca gcc aag gac atc acc ccc acc cta acg Asn His Ser Glu Thr Ala Ser Ala Lys Asp Ile Thr Pro Thr Leu Thr	537
150 155 160	
ctc tac gtg ggg aaa aac cag ctg gtg gag att gag aag gtc gtt ctc Leu Tyr Val Gly Lys Asn Gln Leu Val Glu Ile Glu Lys Val Val Leu	585
165 170 175	
cac ccc aac cac tcc gtg gtg gat atc ggg cta atc aaa ctc aag cag His Pro Asn His Ser Val Val Asp Ile Gly Leu Ile Lys Leu Lys Gln	633
180 185 190 195	
agg gtg ctt gta acc gag aga gtc atg cct atc tgc ctg cct tcc aaa Arg Val Leu Val Thr Glu Arg Val Met Pro Ile Cys Leu Pro Ser Lys	681
200 205 210	
gac tac ata gca cca ggc cgt gtg ggc tac gtg tct ggc tgg ggg cgg Asp Tyr Ile Ala Pro Gly Arg Val Gly Tyr Val Ser Gly Trp Gly Arg	729
215 220 225	
aac gcc aac ttt aga ttt acc gat cgt ctc aag tat gtc atg ctg cct Asn Ala Asn Phe Arg Phe Thr Asp Arg Leu Lys Tyr Val Met Leu Pro	777
230 235 240	
gtg gcc gac cag gac aag tgt gtg gtg cac tat gag aat agt aca gtg Val Ala Asp Gln Asp Lys Cys Val Val His Tyr Glu Asn Ser Thr Val	825
245 250 255	
ccc gag aag aaa aac ttg acg agt ccc gtt ggg gtc cag cct atc ttg Pro Glu Lys Lys Asn Leu Thr Ser Pro Val Gly Val Gln Pro Ile Leu	873
260 265 270 275	
aac gag cac acc ttc tgt gct ggc ctc acc aag tac cag gaa gac acc Asn Glu His Thr Phe Cys Ala Gly Leu Thr Lys Tyr Gln Glu Asp Thr	921
280 285 290	
tgc tac ggt gac gcc ggc agt gcc ttt gcc att cat gac atg gag gag Cys Tyr Gly Asp Ala Gly Ser Ala Phe Ala Ile His Asp Met Glu Glu	969
295 300 305	
gac acc tgg tac gca gct ggg atc ctg agc ttt gac aag agc tgc gct Asp Thr Trp Tyr Ala Ala Gly Ile Leu Ser Phe Asp Lys Ser Cys Ala	1017
310 315 320	
gtc gct gag tat ggt gtg tac gtg agg gcg acc gac ctg aag gac tgg Val Ala Glu Tyr Gly Val Tyr Val Arg Ala Thr Asp Leu Lys Asp Trp	1065
325 330 335	

gtt cag gaa acc atg gcc aag aac tag ttcagggctc actagaaggc 1112
Val Gln Glu Thr Met Ala Lys Asn *
340 345

tgcacatggc agggcaggct gggagccatg gaagaggggg aagtggagg gttgggctat 1172
actctgatgg gttctagccc tgcaactgctc agtcaacaat aaaaaaatgt gctttggacc 1232
cataaaaaaa aaaaaaaaaa aaaaaaaggg aattc 1267

<210> 14
<211> 347
<212> PRT
<213> mouse

<400> 14
Met Arg Ala Leu Gly Ala Val Val Thr Leu Leu Leu Trp Gly Gln Leu 15
1 5 10 15
Phe Ala Val Glu Leu Gly Asn Asp Ala Met Asp Phe Glu Asp Asp Ser 30
20 25 30
Cys Pro Lys Pro Pro Glu Ile Ala Asn Gly Tyr Val Glu His Leu Val 45
35 40 45
Arg Tyr Arg Cys Arg Gln Phe Tyr Arg Leu Arg Ala Glu Gly Asp Gly 60
50 55 60
Val Tyr Thr Leu Asn Asp Glu Lys Gln Trp Val Asn Thr Val Ala Gly 80
65 70 75 80
Glu Lys Leu Pro Glu Cys Glu Ala Val Cys Gly Lys Pro Lys His Pro 95
85 90 95
Val Asp Gln Val Gln Arg Ile Ile Gly Gly Ser Met Asp Ala Lys Gly 110
100 105 110
Ser Phe Pro Trp Gln Ala Lys Met Ile Ser Arg His Gly Leu Thr Thr 125
115 120 125
Gly Ala Thr Leu Ile Ser Asp Gln Trp Leu Leu Thr Thr Ala Lys Asn 140
130 135 140
Leu Phe Leu Asn His Ser Glu Thr Ala Ser Ala Lys Asp Ile Thr Pro 160
145 150 155 160
Thr Leu Thr Leu Tyr Val Gly Lys Asn Gln Leu Val Glu Ile Glu Lys 175
165 170 175
Val Val Leu His Pro Asn His Ser Val Val Asp Ile Gly Leu Ile Lys 190
180 185 190
Leu Lys Gln Arg Val Leu Val Thr Glu Arg Val Met Pro Ile Cys Leu 205
195 200 205
Pro Ser Lys Asp Tyr Ile Ala Pro Gly Arg Val Gly Tyr Val Ser Gly 220
210 215 220
Trp Gly Arg Asn Ala Asn Phe Arg Phe Thr Asp Arg Leu Lys Tyr Val 240
225 230 235 240
Met Leu Pro Val Ala Asp Gln Asp Lys Cys Val Val His Tyr Glu Asn 255
245 250 255
Ser Thr Val Pro Glu Lys Lys Asn Leu Thr Ser Pro Val Gly Val Gln 270
260 265 270
Pro Ile Leu Asn Glu His Thr Phe Cys Ala Gly Leu Thr Lys Tyr Gln 285
275 280 285
Glu Asp Thr Cys Tyr Gly Asp Ala Gly Ser Ala Phe Ala Ile His Asp 300
290 295 300
Met Glu Glu Asp Thr Trp Tyr Ala Ala Gly Ile Leu Ser Phe Asp Lys 320
305 310 315 320
Ser Cys Ala Val Ala Glu Tyr Gly Val Tyr Val Arg Ala Thr Asp Leu 335
325 330 335
Lys Asp Trp Val Gln Glu Thr Met Ala Lys Asn
340 345

<210> 15
<211> 1385
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (70)...(954)

<400> 15
cttgcttggg tttgcagtct tctgcggcag gcattctcg aggaaaccag ccaaggacta 60
actacgacc atg aga ttg gca gtg att tgc ttt tgc ctg ttt ggc att gcc 111
Met Arg Leu Ala Val Ile Cys Phe Cys Leu Phe Gly Ile Ala
1 5 10

tcc	tcc	ctc	ccg	gtg	aaa	gtg	act	gat	tct	ggc	agc	tca	gag	gag	aag	159
Ser	Ser	Leu	Pro	Val	Lys	Val	Thr	Asp	Ser	Gly	Ser	Ser	Glu	Glu	Lys	
15		20				25							30			

ctt	tac	agc	ctg	cac	cca	gat	cct	ata	gcc	aca	tgg	ctg	gtg	cct	gac	207
Leu	Tyr	Ser	Leu	His	Pro	Asp	Pro	Ile	Ala	Thr	Trp	Leu	Val	Pro	Asp	
35								40						45		

cca	tct	cag	aag	cag	aat	ctc	ctt	gcg	cca	cag	aat	gct	gtg	tcc	tct	255
Pro	Ser	Gln	Lys	Gln	Asn	Leu	Leu	Ala	Pro	Gln	Asn	Ala	Val	Ser	Ser	
50								55					60			

gaa	gaa	aag	gat	gac	ttt	aag	caa	gaa	act	ctt	cca	agc	aat	tcc	aat	303
Glu	Glu	Lys	Asp	Asp	Phe	Lys	Gln	Glu	Thr	Leu	Pro	Ser	Asn	Ser	Asn	
65						70							75			

gaa	agc	cat	gac	cac	atg	gac	gac	gat	gat	gac	gat	gat	gat	gac	gat	351
Glu	Ser	His	Asp	His	Met	Asp										
80						85							90			

gga	gac	cat	gca	ggg	agc	gag	gat	tct	gtg	gac	tcg	gat	gaa	tct	gac	399
Gly	Asp	His	Ala	Gly	Ser	Glu	Asp	Ser	Val	Asp	Ser	Asp	Glu	Ser	Asp	
95						100				105			110			

gaa	tct	cac	cat	tcg	gat	gag	tct	gat	gag	acc	gtc	act	gct	agt	aca	447
Glu	Ser	His	His	Ser	Asp	Glu	Ser	Asp	Glu	Thr	Val	Thr	Ala	Ser	Thr	
115						120				125						

caa	gca	gac	act	ttc	act	cca	atc	gtc	cct	aca	gtc	gat	gtc	ccc	aac	495
Gln	Ala	Asp	Thr	Phe	Thr	Pro	Ile	Val	Pro	Thr	Val	Asp	Val	Pro	Asn	
130								135					140			

ggc	cga	ggt	gat	agc	ttg	gct	tat	gga	ctg	agg	tca	aag	tct	agg	agt	543
Gly	Arg	Gly	Asp	Ser	Leu	Ala	Tyr	Gly	Leu	Arg	Ser	Lys	Ser	Arg	Ser	
145								150					155			

ttc	cag	gtt	tct	gat	gaa	cag	tat	cct	gat	gcc	aca	gat	gag	gac	ctc	591
Phe	Gln	Val	Ser	Asp	Glu	Gln	Tyr	Pro	Asp	Ala	Thr	Asp	Glu	Asp	Leu	
160								165					170			

acc	tct	cac	atg	aag	agc	ggt	gag	tct	aag	gag	tcc	ctc	gat	gtc	atc	639
Thr	Ser	His	Met	Lys	Ser	Gly	Glu	Ser	Lys	Glu	Ser	Leu	Asp	Val	Ile	
175						180				185			190			

cct	gtt	gcc	cag	ctt	ctg	agc	atg	ccc	tct	gat	cag	gac	aac	aac	gga	687
Pro	Val	Ala	Gln	Leu	Leu	Ser	Met	Pro	Ser	Asp	Gln	Asp	Asn	Asn	Gly	
195								200					205			

aag	ggc	agc	cat	gag	tca	agt	cag	ctg	gat	gaa	cca	agt	ctg	gaa	aca	735
Lys	Gly	Ser	His	Glu	Ser	Ser	Gln	Leu	Asp	Glu	Pro	Ser	Leu	Glu	Thr	
210								215					220			

cac	aga	ctt	gag	cat	tcc	aaa	gag	agc	cag	gag	agt	gcc	gat	cag	tcg	783
His	Arg	Leu	Glu	His	Ser	Lys	Glu	Ser	Gln	Glu	Ser	Ala	Asp	Gln	Ser	
225								230					235			

gat	gtg	atc	gat	agt	caa	gca	agt	tcc	aaa	gcc	agc	ctg	gaa	cat	cag	831
Asp	Val	Ile	Asp	Ser	Gln	Ala	Ser	Ser	Lys	Ala	Ser	Leu	Glu	His	Gln	
240								245					250			

agc	cac	aag	ttt	cac	agc	cac	aag	gac	aag	cta	gtc	cta	gac	cct	aag	879
Ser	His	Lys	Phe	His	Ser	His	Lys	Asp	Lys	Leu	Val	Leu	Asp	Pro	Lys	
255								260					265			270

agt aag gaa gat gat agg tat ctg aaa ttc cga att tct cat gaa tta 927
Ser Lys Glu Asp Asp Arg Tyr Leu Lys Phe Arg Ile Ser His Glu Leu
275 280 285

gag agt tca tct tct gag gtc aac taa agaagaggca aaaacacagt 974
Glu Ser Ser Ser Glu Val Asn *
290

tccttacttt gcatttagta aaaacaagaa aaagtgttag tgaggattaa gcaggaatac 1034
taactgctca ttctcagt cagtggat atgtatgtag agaaaagagag gtaatatttt 1094
gggctcttag cttagtcgt tgtttcatgc aaacaaccgt tgtaacccaa agcttctgca 1154
ctttgcttct gtcttcctgt tacaagaaaat gcaaacggcc actgcatttt aatgattgtt 1214
attctttat gaataaaaatg tatgtagaaa caagcaaatt tactgaaaca agcagaatta 1274
aaagagaaaac tctaaccgtc tatatcacta tacccttta gtttataat tagcatatat 1334
tttgttgtga ttattttt tgttggtgtg aataaatctt gtaacgaatg t 1385

<210> 16
<211> 294
<212> PRT
<213> mouse

<400> 16
Met Arg Leu Ala Val Ile Cys Phe Cys Leu Phe Gly Ile Ala Ser Ser
1 5 10 15
Leu Pro Val Lys Val Thr Asp Ser Gly Ser Ser Glu Glu Lys Leu Tyr
20 25 30
Ser Leu His Pro Asp Pro Ile Ala Thr Trp Leu Val Pro Asp Pro Ser
35 40 45
Gln Lys Gln Asn Leu Leu Ala Pro Gln Asn Ala Val Ser Ser Glu Glu
50 55 60
Lys Asp Asp Phe Lys Gln Glu Thr Leu Pro Ser Asn Ser Asn Glu Ser
65 70 75 80
His Asp His Met Asp Asp Asp Asp Asp Asp Asp Asp Asp Gly Asp
85 90 95
His Ala Gly Ser Glu Asp Ser Val Asp Ser Asp Glu Ser Asp Glu Ser
100 105 110
His His Ser Asp Glu Ser Asp Glu Thr Val Thr Ala Ser Thr Gln Ala
115 120 125
Asp Thr Phe Thr Pro Ile Val Pro Thr Val Asp Val Pro Asn Gly Arg
130 135 140
Gly Asp Ser Leu Ala Tyr Gly Leu Arg Ser Lys Ser Arg Ser Phe Gln
145 150 155 160
Val Ser Asp Glu Gln Tyr Pro Asp Ala Thr Asp Glu Asp Leu Thr Ser
165 170 175
His Met Lys Ser Gly Glu Ser Lys Glu Ser Leu Asp Val Ile Pro Val
180 185 190
Ala Gln Leu Leu Ser Met Pro Ser Asp Gln Asp Asn Asn Gly Lys Gly
195 200 205
Ser His Glu Ser Ser Gln Leu Asp Glu Pro Ser Leu Glu Thr His Arg
210 215 220
Leu Glu His Ser Lys Glu Ser Gln Glu Ser Ala Asp Gln Ser Asp Val
225 230 235 240
Ile Asp Ser Gln Ala Ser Ser Lys Ala Ser Leu Glu His Gln Ser His
245 250 255
Lys Phe His Ser His Lys Asp Lys Leu Val Leu Asp Pro Lys Ser Lys
260 265 270
Glu Asp Asp Arg Tyr Leu Lys Phe Arg Ile Ser His Glu Leu Glu Ser
275 280 285
Ser Ser Ser Glu Val Asn
290

<210> 17
<211> 725
<212> DNA
<213> human

<220>

<221> CDS
<222> (54) ... (353)

<400> 17
ctaacccaga aacatccaat tctcaaactg aagctcgcac tctgcctcc agc atg 56
Met
1

aaa gtc tct gcc gcc ctt ctg tgc ctg ctg ctc ata gca gcc acc ttc 104
Lys Val Ser Ala Ala Leu Leu Cys Leu Leu Ile Ala Ala Thr Phe
5 10 15

att ccc caa ggg ctc gct cag cca gat gca atc aat gcc cca gtc acc 152
Ile Pro Gln Gly Leu Ala Gln Pro Asp Ala Ile Asn Ala Pro Val Thr
20 25 30

tgc tgt tat aac ttc acc aat agg aag atc tca gtg cag agg ctc gcg 200
Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu Ala
35 40 45

agc tat aga aga atc acc agc agc aag tgt ccc aaa gaa gct gtg atc 248
Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val Ile
50 55 60 65

ttc aag acc att gtg gcc aag gag atc tgt gct gac ccc aag cag aag 296
Phe Lys Thr Ile Val Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys
70 75 80

tgg gtt cag gat tcc atg gac cac ctg gac aag caa acc caa act ccg 344
Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr Pro
85 90 95

aag act tga acactcaactc cacaacccaa gaatctgcag ctaacttatt 393
Lys Thr *

ttcccctagc ttccccaga caccctgttt tattttatta taatgaattt tgtttgtga 453
tgtgaacat tatgccttaa gtaatgttaa ttcttattta agtattgtat gtttaagt 513
tatcttcat ggtactagtg ttttttagat acagagactt gggaaattt cttttctct 573
tgaaccacag ttctaccctt gggatgttt gagggcttt gcaagaatca ttaataaaaa 633
gaatttttt taacattcca atgcattgct aaaatattat tgtggaaatg aatattttgt 693
aactattaca ccaaataaaat atattttgt ac 725

<210> 18
<211> 99
<212> PRT
<213> human

<400> 18
Met Lys Val Ser Ala Ala Leu Leu Cys Leu Leu Ile Ala Ala Thr 1 5 10 15
Phe Ile Pro Gln Gly Leu Ala Gln Pro Asp Ala Ile Asn Ala Pro Val 20 25 30
Thr Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu 35 40 45
Ala Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val 50 55 60
Ile Phe Lys Thr Ile Val Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln 65 70 75 80
Lys Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr 85 90 95
Pro Lys Thr

<210> 19
<211> 584
<212> DNA
<213> mouse

<220>
 <221> CDS
 <222> (89)...(535)

<400> 19
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 gaagccagct ctcttttcct ccaccacc atg cag gtc cct gtc atg ctt ctg 112
 Met Gln Val Pro Val Met Leu Leu
 1 5

ggc ctg ctg ttc aca gtt gcc ggc tgg agc atc cac gtg ttg gct cag 160
 Gly Leu Leu Phe Thr Val Ala Gly Trp Ser Ile His Val Leu Ala Gln
 10 15 20

cca gat gca gtt aac gcc cca ctc acc tgc tgc tac tca ttc acc agc 208
 Pro Asp Ala Val Asn Ala Pro Leu Thr Cys Cys Tyr Ser Phe Thr Ser
 25 30 35 40

aag atg atc cca atg agt agg ctg gag agc tac aag agg atc acc agc 256
 Lys Met Ile Pro Met Ser Arg Leu Glu Ser Tyr Lys Arg Ile Thr Ser
 45 50 55

agc agg tgt ccc aaa gaa gct gta gtt ttt gtc acc aag ctc aag aga 304
 Ser Arg Cys Pro Lys Glu Ala Val Val Phe Val Thr Lys Leu Lys Arg
 60 65 70

gag gtc tgt gct gac ccc aag aag gaa tgg gtc cag aca tac att aaa 352
 Glu Val Cys Ala Asp Pro Lys Lys Glu Trp Val Gln Thr Tyr Ile Lys
 75 80 85

aac ctg gat cgg aac caa atg aga tca gaa cct aca act tta ttt aaa 400
 Asn Leu Asp Arg Asn Gln Met Arg Ser Glu Pro Thr Thr Leu Phe Lys
 90 95 100

act gca tct gcc cta agg tct tca gca cct ttg aat gtg aag ttg acc 448
 Thr Ala Ser Ala Leu Arg Ser Ser Ala Pro Leu Asn Val Lys Leu Thr
 105 110 115 120

cgt aaa tct gaa gct aat gca tcc act acc ttt tcc aca acc acc tca 496
 Arg Lys Ser Glu Ala Asn Ala Ser Thr Thr Phe Ser Thr Thr Ser
 125 130 135

agc act tct gta gga gtg acc agt gtg aca gtg aac tag tgtgactcgg 545
 Ser Thr Ser Val Gly Val Thr Ser Val Thr Val Asn *

140 145

actgtgatgc cttaattaat attaaaactta tttaactta 584

<210> 20
 <211> 148
 <212> PRT
 <213> mouse

<400> 20
 Met Gln Val Pro Val Met Leu Leu Gly Leu Leu Phe Thr Val Ala Gly
 1 5 10 15
 Trp Ser Ile His Val Leu Ala Gln Pro Asp Ala Val Asn Ala Pro Leu
 20 25 30
 Thr Cys Cys Tyr Ser Phe Thr Ser Lys Met Ile Pro Met Ser Arg Leu
 35 40 45
 Glu Ser Tyr Lys Arg Ile Thr Ser Ser Arg Cys Pro Lys Glu Ala Val
 50 55 60
 Val Phe Val Thr Lys Leu Lys Arg Glu Val Cys Ala Asp Pro Lys Lys
 65 70 75 80
 Glu Trp Val Gln Thr Tyr Ile Lys Asn Leu Asp Arg Asn Gln Met Arg
 85 90 95
 Ser Glu Pro Thr Thr Leu Phe Lys Thr Ala Ser Ala Leu Arg Ser Ser
 100 105 110

Ala Pro Leu Asn Val Lys Leu Thr Arg Lys Ser Glu Ala Asn Ala Ser
115 120 125
Thr Thr Phe Ser Thr Thr Ser Ser Thr Ser Val Gly Val Thr Ser
130 135 140
Val Thr Val Asn
145